

Amendments to the Claims

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Claim 1 (Currently amended): A method for identifying ~~an animal~~ a pig with a polymorphism at position 678 of SEQ ID NO:1, wherein a pig with a guanine at position 678 is indicative of said pig more likely to have less back fat, lower daily gain, and lower feed intake than a pig with an adenine at position 678 of SEQ ID NO:1, wherein an adenine is indicative of higher feed intake ~~which possesses a genotype associated with one or more favorable metabolic traits selected from fat content, growth rate, and feed consumption,~~ the method comprising:

~~obtaining a nucleic acid sample from an animal; and~~

~~detecting the nucleotide present a polymorphism at position 678 of SEQ ID NO: 1; and wherein said polymorphism is associated with one or more of the metabolic traits of fat content, growth rate, and feed consumption~~

relating the polymorphism to the phenotype.

Claim 2 (Previously presented): The method of claim 1 wherein the polymorphism is detected at position 678 of a PCR sequence using a forward primer and a reverse.

Claims 3-6 (Cancelled)

Claim 7 (Currently amended): The method of claim 1 wherein the step of ~~identifying~~ detecting the polymorphism is a method employing allele specific oligonucleotides.

Claim 8 (Currently amended): The method of claim 1 wherein the step of ~~identifying~~ detecting the polymorphism is selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), and use of linked genetic markers.

Claim 9 (Currently amended): The method of claim 8 wherein the step of ~~identifying~~ detecting the polymorphism comprises RFLP analysis.